

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/581,223  
Source: TFWP  
Date Processed by STIC: 6/9/06

# ***ENTERED***



IFWP

## RAW SEQUENCE LISTING

DATE: 06/09/2006

PATENT APPLICATION: US/10/581,223

TIME: 10:38:51

Input Set : A:\Final Sequence list-12810-00260-US.txt

Output Set: N:\CRF4\06092006\J581223.raw

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3 <110> APPLICANT: Ehrhardt, Thomas
4      Reindl, Andreas
5      Freund, Annette
6      Schmidt, Ralf-Michael
7      Sonnewald, Uwe
8      Sitt Nigel, Marc
9      Lein, Wolfgang
10     Bornke, Frederik
12 <120> TITLE OF INVENTION: 2-Methyl-6-solanylbenzoquinone methyltransferase as target
for
13     herbicides
15 <130> FILE REFERENCE: 12810-00260-US
C--> 17 <140> CURRENT APPLICATION NUMBER: US/10/581,223
C--> 17 <141> CURRENT FILING DATE: 2006-06-01
17 <150> PRIOR APPLICATION NUMBER: PCT/EP2004/013560
18 <151> PRIOR FILING DATE: 2004-11-30
20 <150> PRIOR APPLICATION NUMBER: DE 103 56 631.7
21 <151> PRIOR FILING DATE: 2003-12-02
23 <160> NUMBER OF SEQ ID NOS: 35
25 <170> SOFTWARE: PatentIn version 3.3
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 1355
30 <212> TYPE: DNA
31 <213> ORGANISM: Nicotiana tabacum
33 <220> FEATURE:
34 <221> NAME/KEY: CDS
35 <222> LOCATION: (110)..(1117)
38 <400> SEQUENCE: 1
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41 ttatcaaaac tatatgcagt aaaaaaata acatcaaaaa tacatatcc atg gct tct      118
42                                     Met Ala Ser
43                                     1
45 tca ata cta agt gga gct gaa aat ttc aag att ctt agt ggt att tct      166
46 Ser Ile Leu Ser Gly Ala Glu Asn Phe Lys Ile Leu Ser Gly Ile Ser
47      5              10              15
49 cca tca gaa tta cac att aag tgt ttt cct caa aag ggt ctt gta aat      214
50 Pro Ser Glu Leu His Ile Lys Cys Phe Pro Gln Lys Gly Leu Val Asn
51 20              25              30              35
53 tac tca aga att cca aat acc aaa tca aga act cta aga aca aaa tgc      262
54 Tyr Ser Arg Ile Pro Asn Thr Lys Ser Arg Thr Leu Arg Thr Lys Cys
55      40              45              50
57 agt gta tca tct tca aga cca gct tca caa cca aga ttt ata caa cac      310
58 Ser Val Ser Ser Ser Arg Pro Ala Ser Gln Pro Arg Phe Ile Gln His
59      55              60              65

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61 aaa aaa gaa gca ttt tgg ttt tac aga ttc tta tct ata gta tat gac      358
62 Lys Lys Glu Ala Phe Trp Phe Tyr Arg Phe Leu Ser Ile Val Tyr Asp
63      70      75      80
65 cat gtt ata aat cca ggt cat tgg act gaa gat atg aga gat gaa gca      406
66 His Val Ile Asn Pro Gly His Trp Thr Glu Asp Met Arg Asp Glu Ala
67      85      90      95
69 ctt gaa cca gct gaa tta aac agt aga caa ttg caa gtt gtg gat gtt      454
70 Leu Glu Pro Ala Glu Leu Asn Ser Arg Gln Leu Gln Val Val Asp Val
71 100      105      110      115
73 ggt ggt ggg act gga ttt act act ctt ggc att gtg aaa cat gtg gat      502
74 Gly Gly Gly Thr Gly Phe Thr Thr Leu Gly Ile Val Lys His Val Asp
75      120      125      130
77 gct aag aat gtt aca att att gat caa tca cct cat caa ctt gcc aag      550
78 Ala Lys Asn Val Thr Ile Ile Asp Gln Ser Pro His Gln Leu Ala Lys
79      135      140      145
81 gct aga gaa aag gaa cct ttg aaa gaa tgt aag ata ttg gaa gga gat      598
82 Ala Arg Glu Lys Glu Pro Leu Lys Glu Cys Lys Ile Leu Glu Gly Asp
83      150      155      160
85 gct gag gat ttg cct ttt cct act gat act ttt gat aga tat gtt tct      646
86 Ala Glu Asp Leu Pro Phe Pro Thr Asp Thr Phe Asp Arg Tyr Val Ser
87      165      170      175
89 gct gga agc att gag tat tgg ccc gat cca cag cgc ggt atc aag gaa      694
90 Ala Gly Ser Ile Glu Tyr Trp Pro Asp Pro Gln Arg Gly Ile Lys Glu
91 180      185      190      195
93 gca tac cga gta ctg acc ata ggt ggt gtt gcc tgc tta ata ggt cct      742
94 Ala Tyr Arg Val Leu Thr Ile Gly Gly Val Ala Cys Leu Ile Gly Pro
95      200      205      210
97 gtg tac ccg acg ttt tgg cta tct cgt ttc ttt gca gat atg tgg atg      790
98 Val Tyr Pro Thr Phe Trp Leu Ser Arg Phe Phe Ala Asp Met Trp Met
99      215      220      225
101 ctc ttt cca aaa gaa gaa gaa tat ata gaa tgg ttc aaa aaa gct ggt      838
102 Leu Phe Pro Lys Glu Glu Glu Tyr Ile Glu Trp Phe Lys Lys Ala Gly
103      230      235      240
105 ttc gct caa gtt aaa ctc aag agg att ggc cca aaa tgg tat cgt ggt      886
106 Phe Ala Gln Val Lys Leu Lys Arg Ile Gly Pro Lys Trp Tyr Arg Gly
107      245      250      255
109 gtc cgt cgc cat ggc ttg atc atg ggt tgt tct gtg act ggt gtc aag      934
110 Val Arg Arg His Gly Glu Ile Met Gly Cys Ser Val Thr Gly Val Lys
111 260      265      270      275
113 cca tat ttt ggg gaa tct ccg ttg cag ctc ggc ccg aag gtt gag gat      982
114 Pro Tyr Phe Gly Glu Ser Pro Leu Gln Leu Gly Pro Lys Val Glu Asp
115      280      285      290
117 gtg agc aag cct gta aac cca ttc gca ttt ctc gtg cga ttc ctc ctc      1030
118 Val Ser Lys Pro Val Asn Pro Phe Ala Phe Leu Val Arg Phe Leu Leu
119      295      300      305
121 ggc ata act gct gca act tat tac gtg ctc gtt cca ata tac atg tgg      1078
122 Gly Ile Thr Ala Ala Thr Tyr Tyr Val Leu Val Pro Ile Tyr Met Trp
123      310      315      320
125 ctc aag gat caa atc acc ccg aaa ggt cag cca atc tga acaataagaa      1127

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126 Leu Lys Asp Gln Ile Thr Pro Lys Gly Gln Pro Ile
127      325      330      335
129 gaacgtcaat ccaaagagaa gctctccaag cattctgttt gagagtacac cagtgaccac 1187
131 aaatctatca cggaacaaga aagtttttgg cgtcgttgca aggggtgaatt tgttgcttta 1247
133 gtttgtagt tttgcagcct tagaaagggc cttttgtaaa gtttaatttc atggtaaaac 1307
135 ctagaaatca ttgtgactat tttctagttg tataatctat cagtcatg 1355
138 <210> SEQ ID NO: 2
139 <211> LENGTH: 335
140 <212> TYPE: PRT
141 <213> ORGANISM: Nicotiana tabacum
143 <400> SEQUENCE: 2
145 Met Ala Ser Ser Ile Leu Ser Gly Ala Glu Asn Phe Lys Ile Leu Ser
146 1      5      10      15
149 Gly Ile Ser Pro Ser Glu Leu His Ile Lys Cys Phe Pro Gln Lys Gly
150      20      25      30
153 Leu Val Asn Tyr Ser Arg Ile Pro Asn Thr Lys Ser Arg Thr Leu Arg
154      35      40      45
157 Thr Lys Cys Ser Val Ser Ser Ser Arg Pro Ala Ser Gln Pro Arg Phe
158 50      55      60
161 Ile Gln His Lys Lys Glu Ala Phe Trp Phe Tyr Arg Phe Leu Ser Ile
162 65      70      75      80
165 Val Tyr Asp His Val Ile Asn Pro Gly His Trp Thr Glu Asp Met Arg
166      85      90      95
169 Asp Glu Ala Leu Glu Pro Ala Glu Leu Asn Ser Arg Gln Leu Gln Val
170      100     105     110
173 Val Asp Val Gly Gly Gly Thr Gly Phe Thr Thr Leu Gly Ile Val Lys
174      115     120     125
177 His Val Asp Ala Lys Asn Val Thr Ile Ile Asp Gln Ser Pro His Gln
178      130     135     140
181 Leu Ala Lys Ala Arg Glu Lys Glu Pro Leu Lys Glu Cys Lys Ile Leu
182 145     150     155     160
185 Glu Gly Asp Ala Glu Asp Leu Pro Phe Pro Thr Asp Thr Phe Asp Arg
186      165     170     175
189 Tyr Val Ser Ala Gly Ser Ile Glu Tyr Trp Pro Asp Pro Gln Arg Gly
190      180     185     190
193 Ile Lys Glu Ala Tyr Arg Val Leu Thr Ile Gly Gly Val Ala Cys Leu
194      195     200     205
197 Ile Gly Pro Val Tyr Pro Thr Phe Trp Leu Ser Arg Phe Phe Ala Asp
198      210     215     220
201 Met Trp Met Leu Phe Pro Lys Glu Glu Glu Tyr Ile Glu Trp Phe Lys
202 225     230     235     240
205 Lys Ala Gly Phe Ala Gln Val Lys Leu Lys Arg Ile Gly Pro Lys Trp
206      245     250     255
209 Tyr Arg Gly Val Arg Arg His Gly Leu Ile Met Gly Cys Ser Val Thr
210      260     265     270
213 Gly Val Lys Pro Tyr Phe Gly Glu Ser Pro Leu Gln Leu Gly Pro Lys
214      275     280     285
217 Val Glu Asp Val Ser Lys Pro Val Asn Pro Phe Ala Phe Leu Val Arg
218      290     295     300

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221 Phe Leu Leu Gly Ile Thr Ala Ala Thr Tyr Tyr Val Leu Val Pro Ile
222 305                      310                      315                      320
225 Tyr Met Trp Leu Lys Asp Gln Ile Thr Pro Lys Gly Gln Pro Ile
226                      325                      330                      335
229 <210> SEQ ID NO: 3
230 <211> LENGTH: 1017
231 <212> TYPE: DNA
232 <213> ORGANISM: Arabidopsis thaliana
234 <220> FEATURE:
235 <221> NAME/KEY: CDS
236 <222> LOCATION: (1)..(1017)
238 <400> SEQUENCE: 3
240 atg gcc tct ttg atg ctc aac ggg gcc att acc ttc ccc aaa ggt tta      48
241 Met Ala Ser Leu Met Leu Asn Gly Ala Ile Thr Phe Pro Lys Gly Leu
242 1                      5                      10                      15
244 ggt tcc cct ggt tcc aat ttg cat gcc aaa tcg att cct cgg ccg acc      96
245 Gly Ser Pro Gly Ser Asn Leu His Ala Lys Ser Ile Pro Arg Pro Thr
246                      20                      25                      30
248 tta ctc tca gtt acc cga acc tcc aca cct aga ctc tcg gtg gct act     144
249 Leu Leu Ser Val Thr Arg Thr Ser Thr Pro Arg Leu Ser Val Ala Thr
250                      35                      40                      45
252 aaa tgc agc agc agc agc gtg tcg tct tcc cgg cca tcg gcg caa cct     192
253 Lys Cys Ser Ser Ser Ser Val Ser Ser Ser Arg Pro Ser Ala Gln Pro
254 50                      55                      60
256 agg ttc att cag cac aag aag gag gct tac tgg ttc tac agg ttc tta     240
257 Arg Phe Ile Gln His Lys Lys Glu Ala Tyr Trp Phe Tyr Arg Phe Leu
258 65                      70                      75                      80
260 tcc atc gta tac gac cat gtc atc aat cct ggg cat tgg acc gag gat     288
261 Ser Ile Val Tyr Asp His Val Ile Asn Pro Gly His Trp Thr Glu Asp
262                      85                      90                      95
264 atg aga gac gac gct ctt gag cca gcg gat ctc agc cat ccg gac atg     336
265 Met Arg Asp Asp Ala Leu Glu Pro Ala Asp Leu Ser His Pro Asp Met
266                      100                     105                     110
268 cga gtg gtc gat gtc ggc ggc gga act ggt ttc act act ctg ggc ata     384
269 Arg Val Val Asp Val Gly Gly Gly Thr Gly Phe Thr Thr Leu Gly Ile
270                      115                     120                     125
272 gtc aag aca gtg aag gcc aag aat gtg acc att ctg gac cag tcg cca     432
273 Val Lys Thr Val Lys Ala Lys Asn Val Thr Ile Leu Asp Gln Ser Pro
274                      130                     135                     140
276 cat cag ctg gcc aaa gca aag caa aag gag ccg ttg aaa gaa tgc aag     480
277 His Gln Leu Ala Lys Ala Lys Gln Lys Glu Pro Leu Lys Glu Cys Lys
278 145                      150                     155                     160
280 atc gtc gag gga gat gct gag gat ctt cct ttt cca acc gat tat gct     528
281 Ile Val Glu Gly Asp Ala Glu Asp Leu Pro Phe Pro Thr Asp Tyr Ala
282                      165                     170                     175
284 gac aga tac gtt tct gct gga agc att gag tac tgg ccg gac ccg cag     576
285 Asp Arg Tyr Val Ser Ala Gly Ser Ile Glu Tyr Trp Pro Asp Pro Gln
286                      180                     185                     190
288 agg gga ata agg gaa gcg tac agg gtt ctc aag atc ggt ggc aaa gcg     624

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289 Arg Gly Ile Arg Glu Ala Tyr Arg Val Leu Lys Ile Gly Gly Lys Ala
290      195      200      205
292 tgt ctc atc ggc cct gtc tac cca acc ttc tgg ctc tct cgc ttc ttt      672
293 Cys Leu Ile Gly Pro Val Tyr Pro Thr Phe Trp Leu Ser Arg Phe Phe
294      210      215      220
296 tct gat gtc tgg atg ctc ttc ccc aag gag gaa gag tac att gag tgg      720
297 Ser Asp Val Trp Met Leu Phe Pro Lys Glu Glu Glu Tyr Ile Glu Trp
298 225      230      235      240
300 ttc aag aat gcc ggt ttc aag gac gtt cag ctc aag agg att ggc ccc      768
301 Phe Lys Asn Ala Gly Phe Lys Asp Val Gln Leu Lys Arg Ile Gly Pro
302      245      250      255
304 aag tgg tac cgt ggt gtt cgc agg cac ggc ctt atc atg gga tgt tct      816
305 Lys Trp Tyr Arg Gly Val Arg Arg His Gly Leu Ile Met Gly Cys Ser
306      260      265      270
308 gtc act ggt gtt aaa cct gcc tcc ggt gat tct cct ctc cag ctt ggt      864
309 Val Thr Gly Val Lys Pro Ala Ser Gly Asp Ser Pro Leu Gln Leu Gly
310      275      280      285
312 cca aag gaa gag gac gta gag aag cct gtc aac aac ccc ttc tcc ttc      912
313 Pro Lys Glu Glu Asp Val Glu Lys Pro Val Asn Asn Pro Phe Ser Phe
314      290      295      300
316 ttg gga cgc ttc ctc ctg gga act cta gca gct gcc tgg ttt gtg tta      960
317 Leu Gly Arg Phe Leu Gly Thr Leu Ala Ala Trp Phe Val Leu
318 305      310      315      320
320 atc cct atc tac atg tgg atc aag gat cag atc gtt ccc aaa gac caa      1008
321 Ile Pro Ile Tyr Met Trp Ile Lys Asp Gln Ile Val Pro Lys Asp Gln
322      325      330      335
324 ccc atc tga      1017
325 Pro Ile
329 <210> SEQ ID NO: 4
330 <211> LENGTH: 338
331 <212> TYPE: PRT
332 <213> ORGANISM: Arabidopsis thaliana
334 <400> SEQUENCE: 4
336 Met Ala Ser Leu Met Leu Asn Gly Ala Ile Thr Phe Pro Lys Gly Leu
337 1      5      10      15
340 Gly Ser Pro Gly Ser Asn Leu His Ala Lys Ser Ile Pro Arg Pro Thr
341      20      25      30
344 Leu Leu Ser Val Thr Arg Thr Ser Thr Pro Arg Leu Ser Val Ala Thr
345      35      40      45
348 Lys Cys Ser Ser Ser Ser Val Ser Ser Ser Arg Pro Ser Ala Gln Pro
349      50      55      60
352 Arg Phe Ile Gln His Lys Lys Glu Ala Tyr Trp Phe Tyr Arg Phe Leu
353 65      70      75      80
356 Ser Ile Val Tyr Asp His Val Ile Asn Pro Gly His Trp Thr Glu Asp
357      85      90      95
360 Met Arg Asp Asp Ala Leu Glu Pro Ala Asp Leu Ser His Pro Asp Met
361      100      105      110
364 Arg Val Val Asp Val Gly Gly Gly Thr Gly Phe Thr Thr Leu Gly Ile
365      115      120      125

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**VERIFICATION SUMMARY**

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Input Set : A:\Final Sequence list-12810-00260-US.txt

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L:17 M:270 C: Current Application Number differs, Replaced Current Application No

L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date